Input file Fbh62112FL.seq; Output File 62112.trans
Sequenc length 2452

```
                                                
```

```
GTG TTC AGC TCC GAG GCC GCC TGG CAG TGT GTG AGT GAG GCG CTG CAG ATC CTC GGG GGC  1209

 L   G   Y   T   R   D   Y   P   Y   E   R   I   L   R   D   T   R   I   L   L   423
TTG GGC TAC ACA AGG GAC TAT CCG TAC GAG CGC ATA CTG CGT GAC ACC CGC ATC CTC CTC  1269

 I   F   E   G   T   N   E   I   L   R   M   Y   I   A   L   T   G   L   Q   H   443
ATC TTC GAG GGA ACC AAT GAG ATT CTC CGG ATG TAC ATC GCC CTG ACG GGT CTG CAG CAT  1329

 A   G   R   I   L   T   T   R   I   H   E   L   K   Q   A   K   V   S   T   V   463
GCC GGC CGC ATC CTG ACT ACC AGG ATC CAT GAG CTT AAA CAG GCC AAA GTG AGC ACA GTC  1389

 M   D   T   V   G   R   R   L   R   D   S   L   G   R   T   V   D   L   G   L   483
ATG GAT ACC GTT GGC CGG AGG CTT CGG GAC TCC CTG GGC CGA ACT GTG GAC CTG GGG CTG  1449

 T   G   N   H   G   V   V   H   P   S   L   A   D   S   A   N   K   F   E   E   503
ACA GGC AAC CAT GGA GTT GTG CAC CCC AGT CTT GCG GAC AGT GCC AAC AAG TTT GAG GAG  1509

 N   T   Y   C   F   G   R   T   V   E   T   L   L   L   R   F   G   K   T   I   523
AAC ACC TAC TGC TTC GGC CGG ACC GTG GAG ACA CTG CTG CTC CGC TTT GGC AAG ACC ATC  1569

 M   E   E   Q   L   V   L   K   R   V   A   N   I   L   I   N   L   Y   G   M   543
ATG GAG GAG CAG CTG GTA CTG AAG CGG GTG GCC AAC ATC CTC ATC AAC CTG TAT GGC ATG  1629

 T   A   V   L   S   R   A   S   R   S   I   R   I   G   L   R   N   H   D   H   563
ACG GCC GTG CTG TCG CGG GCC AGC CGC TCC ATC CGC ATT GGG CTC CGC AAC CAC GAC CAC  1689

 E   V   L   L   A   N   T   F   C   V   E   A   Y   L   Q   N   L   F   S   L   583
GAG GTT CTC TTG GCC AAC ACC TTC TGC GTG GAA GCT TAC TTG CAG AAT CTC TTC AGC CTC  1749

 S   Q   L   D   K   Y   A   P   E   N   L   D   E   Q   I   K   K   V   S   Q   603
TCT CAG CTG GAC AAG TAT GCT CCA GAA AAC CTA GAT GAG CAG ATT AAG AAA GTG TCC CAG  1809

 Q   I   L   E   K   R   A   Y   I   C   A   H   P   L   D   R   T   C   *       622
CAG ATC CTT GAG AAG CGA GCC TAT ATC TGT GCC CAC CCT CTG GAC AGG ACA TGC TGA      1866

GGCAGGGGACAGTGTCCCCTGCTACCGCCCGCCCCTACCCATGGCCCGTTGCTGGATGACTGTTACTCTTTTTTCAGAA

GGTGTTGGGATTATCACAGGTTAAGCCTTTTGTTCCCCGTCTGCACCTGAAGGGTTGTCGCCTGGCCTGGGAGAGCCTC

TTCCAGGTTTTGACCTGCAGGCAGTGCTCTCTAACAGGACCATCACAGCTTCTGAACTGAGCCGGAGAGAGAGAATGGA

ATTGCTGACCCCTGGAACTGGCGGGTATTCTGGTCATTGAGGAGACACCATAGTGGAAACTGGGGCTTATGCTGCTGCC

TCCAGGGTGTGAGGTGGGTGGGGACCTGTGTCAGGTGTGGATAGCCATTTCTGCTCAACCACACATTCTCTAAGAAACA

GCTTGAAAGCTCTGTCTGGGTCATTCATTTAAACTAGAAGCAGAGGCACTTAAAACATGTACCAGGAACCATTTAACAA

AGAATATAAAATGTCACAATCTGTGTACTGTTAAAAAAAAAAAAAA
```

FIGURE 1B

```
Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:                 /prod/ddm/seqanal/PFAM/pfam6.4/Pfam
Sequence file:            /prod/ddm/wspace/orfanal/oa-script.26629.seq
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
 Query:  62112

Scores for sequence family classification (score includes all domains):
Model          Description                                  Score    E-value  N
--------       -----------                                  -----    ------- ---
Acyl-CoA_dh_M   Acyl-CoA dehydrogenase, middle domain        153.0     3.5e-42
1
Acyl-CoA_dh     Acyl-CoA dehydrogenase, C-terminal dom       152.1     9.6e-42
1
Acyl-CoA_dh_N   Acyl-CoA dehydrogenase, N-terminal dom        73.7     4.2e-19
1
Polysac_deacet  Polysaccharide deacetylase                   -43.7         1.8
1

Parsed for domains:
Model          Domain  seq-f seq-t    hmm-f hmm-t      score  E-value
--------       ------- ----- -----    ----- -----      -----  -------
Acyl-CoA_dh_N    1/1      85   177 ..    29   132 .]    73.7  4.2e-19
Acyl-CoA_dh_M    1/1     179   286 ..     1   106 []   153.0  3.5e-42
Acyl-CoA_dh      1/1     290   441 ..     1   156 []   152.1  9.6e-42
Polysac_deacet   1/1     432   580 ..     1   150 []   -43.7      1.8

Alignments of top-scoring domains:
Acyl-CoA_dh_N: domain 1 of 1, from 85 to 177: score 73.7, E = 4.2e-19
                   *->RRvDksgefPalrelikaLgqlGllginvPEeyGGaGad..ylaRFm
                      R++D++g+ P   e +++L  lGl+g+ vPEeyGG+G +++ ++
       62112    85 ---RKIDQEGKIP--DETLEKLKSLGLFGLQVPEEYGGLGFSntMYS--- 126

                   LHAQVaalviEElarvcAstgvilsvhssLgqnpilkfGseEQKkkyLpq
                            + E+   ++s  v+l++h ++g+ +i+ +G+eEQK+kyLp+
       62112   127 --------RLGEIISMDGSITVTLAAHQAIGLKGIILAGTEEQKAKYLPK 168

                   ltsGdliga<-*
                   l+sG++i+a
       62112   169 LASGEHIAA    177

Acyl-CoA_dh_M: domain 1 of 1, from 179 to 286: score 153.0, E = 3.5e-42
                   *->AlTEPgAGSDvgSlkTtAekkEGd..dyiLNGsKmWITNGgqAdwyi
                      +lTEP +GSD++S++ +A+    d+++yiLNGsK+WITNGg A++++
       62112   179    CLTEPASGSDAASIRSRATLS-EDkkHYILNGSKVWITNGGLANIFT 224

                   VlAvT...DpakkvpgkkgitaFlVekdtpGfsiGkKedKLGlRgSdTcE
                   V+A+T+  D +   + k  itaF+Ve+d+ G++ Gk+edKLG+RgS+TcE
       62112   225 VFAKTevvDSDG--SVKDKITAFIVERDFGGVTNGKPEDKLGIRGSNTCE 272

                   LiFEDvrvPesniL<-*
                   + FE+ ++P +niL
       62112   273 VHFENTKIPVENIL    286

Acyl-CoA_dh: domain 1 of 1, from 290 to 441: score 152.1, E = 9.6e-42
                   *->GkGFkyamkeLdmeRlviAaqalGlaqgaldeAinYakqRkqFGkpl
                      G+GFk+am+ L+ +R+  +++  Gl+ + ++ +++Ya  RkqF k+l
       62112   290    GDGFKVAMNILNSGRFSMGSVVAGLLKRLIEMTAEYACTRKQFNKRL 336
```

FIGURE 2A

```
                adfQliQfkLAdMatkLEaaRllvYraAwladr.GedAKEALptskeaam
                 +f liQ+k+A Ma k  ++ +++Y +A   d++G +     ++s eaam
       62112   337 SEFGLIQEKFALMAQKAYVMESMTYLTAGMLDQpGFP-----DCSIEAAM 381

                AKlfaseaAmqvatdAvQilGGvGYtkdyPveRfyRDAkitqIYEGTsEI
                +K f+seaA q +++A+QilGG GYt dyP eR +RD +i  I EGT+EI
       62112   382 VKVFSSEAAWQCVSEALQILGGLGYTRDYPYERILRDTRILLIFEGTNEI 431

                qrlvIaRall<-*
                 r  Ia + l
       62112   432 LRMYIALTGL    441

Polysac_deacet: domain 1 of 1, from 432 to 580: score -43.7, E = 1.8
                *->ddksvyLTFDDGPnAApayTprlLDvLkkhkvkATFFviGsnvkdnP
                    +++++LT  + ++  +  T+r+ + Lk+ kv   +   G++ +d
       62112   432    LRMYIALTGLQHAG--RILTTRI-HELKQAKVSTVMDTVGRRLRD-- 473

                dlarrivkeGHeigNHtwsHPdlt.....................tl
                  + r v+ G   gNH+  HP l+++ ++ ++++   +++ ++   +  +
       62112   474 -SLGRTVDLG-LTGNHGVVHPSLAdsankfeentycfgrtvetlllrfGK 521

                taeqirdeiertneaiiqatggatptlfRpPYGewsetvlsasaklGlaa
                t  +++  + r++++++i+++g  t++l R+          s+s ++Gl+
       62112   522 TIMEEQLVLKRVANILINLYG-MTAVLSRA----------SRSIRIGLRN 560

                vlWdvDprDWsvragadaivdavlqaa<-*
                +       D  v   ++  v a+lq+
       62112   561 H-------DHEVLLANTFCVEAYLQNL    580
```

FIGURE 2B

Protein Family / Domain Matches, HMMer version 2

```
Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:                 /prod/ddm/seqanal/PFAM/pfam5.4/Pfam
Sequence file:            /prod/ddm/wspace/orfanal/oa-script.17193.seq
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
 Query:  62112

Scores for sequence family classification (score includes all domains):
Model           Description                                   Score    E-value  N
--------        -----------                                   -----    ------- ---
Acyl-CoA_dh     Acyl-CoA dehydrogenase                         399.8   1.8e-116   1
Polysac_deacet  Polysaccharide deacetylase                     -43.7          1   1

Parsed for domains:
Model           Domain  seq-f seq-t    hmm-f hmm-t       score  E-value
--------        ------- ----- -----    ----- -----       -----  -------
Acyl-CoA_dh       1/1      85   438 ..    29   394 .]    399.8 1.8e-116
Polysac_deacet    1/1     432   580 ..     1   150 []    -43.7         1

Alignments of top-scoring domains:
Acyl-CoA_dh: domain 1 of 1, from 85 to 438: score 399.8, E = 1.8e-116
                 *->RRvDksgefPlrelikaLgklGllginvPEeyGGaGad..ylaRFmL
                    R++D++g+ P  e +++L  lGl+g+ vPEeyGG+G +++ ++
   62112    85     RKIDQEGKIP-DETLEKLKSLGLFGLQVPEEYGGLGFSntMYS---- 126

                    HAQVaalviEElarvcAstgvllsvhssLgqnpilrfGseEQkkkyLpql
                             + E+   ++s  v+l++h ++g+  i+ +G+eEQk+kyLp+l
   62112    127 -------RLGEIISMDGSITVTLAAHQAIGLKGIILAGTEEQKAKYLPKL 169

                    tsGdligafAlTEPgAGSDvgSikTtAekkEGd..dyiLNGsKmWITNGg
```

FIGURE 2C

```
                +sG++i+af+lTEP +GSD++Si+ +A+     d+++yiLNGsK+WITNGg
62112    170 ASGEHIAAFCLTEPASGSDAASIRSRATLS-EDkkHYILNGSKVWITNGG 218

                qAdwyiVlAvT...DpakkvpgkkgitaflvekdtpGfsiGkKedKLGlR
                 A++++V+A+T+  D +    + k  itaF+Ve+d+ G++ Gk+edKLG+R
62112    219 LANIFTVFAKTevvDSDG--SVKDKITAFIVERDFGGVTNGKPEDKLGIR 266

                gSdTcELiFEDvrvPesniLGeEGeGFkyaMktLdmeRlgiAaqalGiaq
                gS+TcE+ FE+ ++P +niLGe G+GFk+aM+ L+ +R+  +++  G++
62112    267 GSNTCEVHFENTKIPVENILGEVGDGFKVAMNILNSGRFSMGSVVAGLLK 316

                gAldeAinYAkqRkqFGkplaefQliQfkLAdMAtkLEaaRllvYraAwl
                + ++ +++YA  RkqF k+l ef liQ+k+A MA k  ++ +++Y ++A
62112    317 RLIEMTAEYACTRKQFNKRLSEFGLIQEKFALMAQKAYVMESMTYLTAGM 366

                adr.GedAKEALptskeAAMAKlfAseiAmkvatdAvQilGGvGYtkdyP
                 d++G +      ++s eAAM+K f+se+A + +++A+QilGG GYt dyP
62112    367 LDQpGFP-----DCSIEAAMVKVFSSEAAWQCVSEALQILGGLGYTRDYP 411

                veRfyRDAkitqIYEGTsEIQrlvIaR<-*
                 eR +RD +i  I EGT+EI r  Ia
62112    412 YERILRDTRILLIFEGTNEILRMYIAL    438

Polysac_deacet: domain 1 of 1, from 432 to 580: score -43.7, E = 1
                *->ddksvyLTFDDGPnAApayTprlLDvLkkhkvkATFFviGsnvkdnP
                    +++++LT  + ++  +  T+r+ + Lk+ kv   +   G++ +d
62112    432    LRMYIALTGLQHAG--RILTTRI-HELKQAKVSTVMDTVGRRLRD-- 473

                dlarrivkeGHeigNHtwsHPdlt.....................tl
                  + r v+ G   gNH+  HP l+++ ++ ++++   +++ ++   +  +
62112    474 -SLGRTVDLG-LTGNHGVVHPSLAdsankfeentycfgrtvetlllrfGK 521

                taeqirdeiertneaiiqatggatptlfRpPYGewsetvlsasaklGlta
                t  +++  + r++++++i+++g  t++l R+          s+s ++Gl+
62112    522 TIMEEQLVLKRVANILINLYG-MTAVLSRA----------SRSIRIGLRN 560

                vlWdvDprDWsvragadaivdavlqaa<-*
                +       D  v   ++  v a+lq+
62112    561 H-------DHEVLLANTFCVEAYLQNL    580
```

FIGURE 2D

TxP expression: 30K array

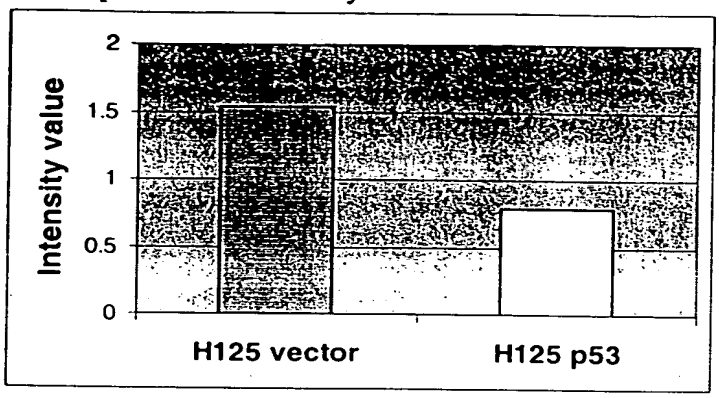


FIGURE 3A

Taqman expression

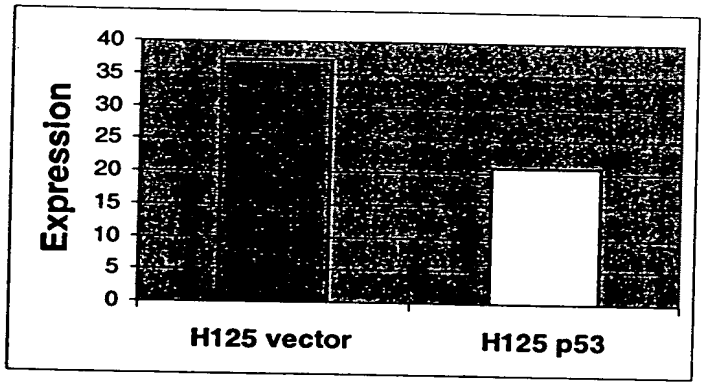
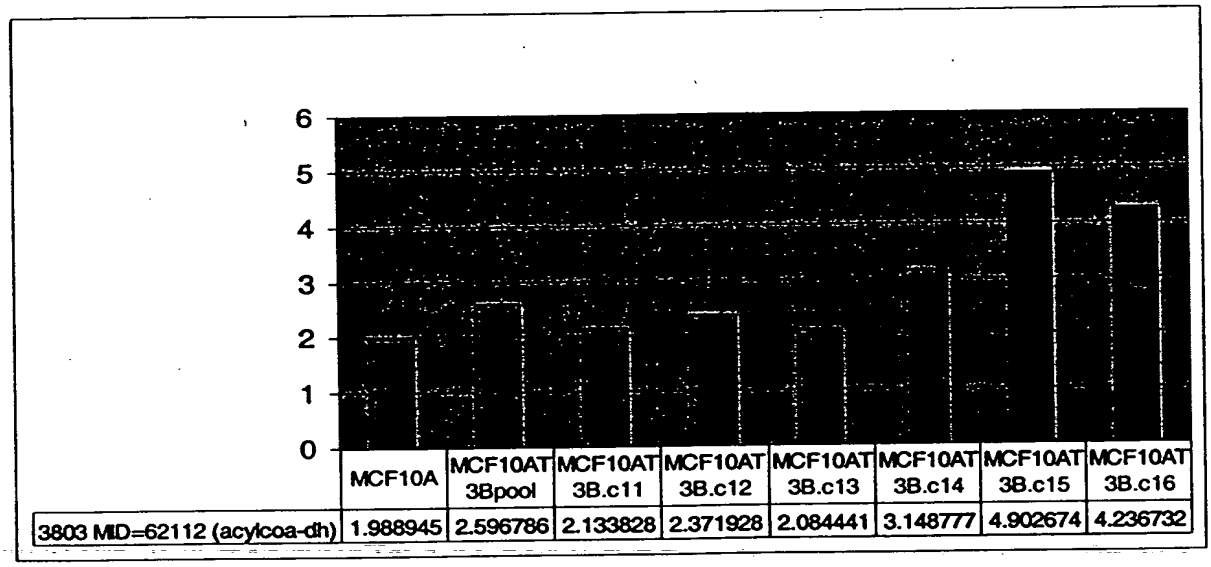


FIGURE 3B

09545526 - 083101



	MCF10A	MCF10AT 3Bpool	MCF10AT 3B.c11	MCF10AT 3B.c12	MCF10AT 3B.c13	MCF10AT 3B.c14	MCF10AT 3B.c15	MCF10AT 3B.c16
3803 MID=62112 (acylcoa-dh)	1.988945	2.596786	2.133828	2.371928	2.084441	3.148777	4.902674	4.236732

09456926 - 083404

FIGURE 4

TOTE80"92ES4660

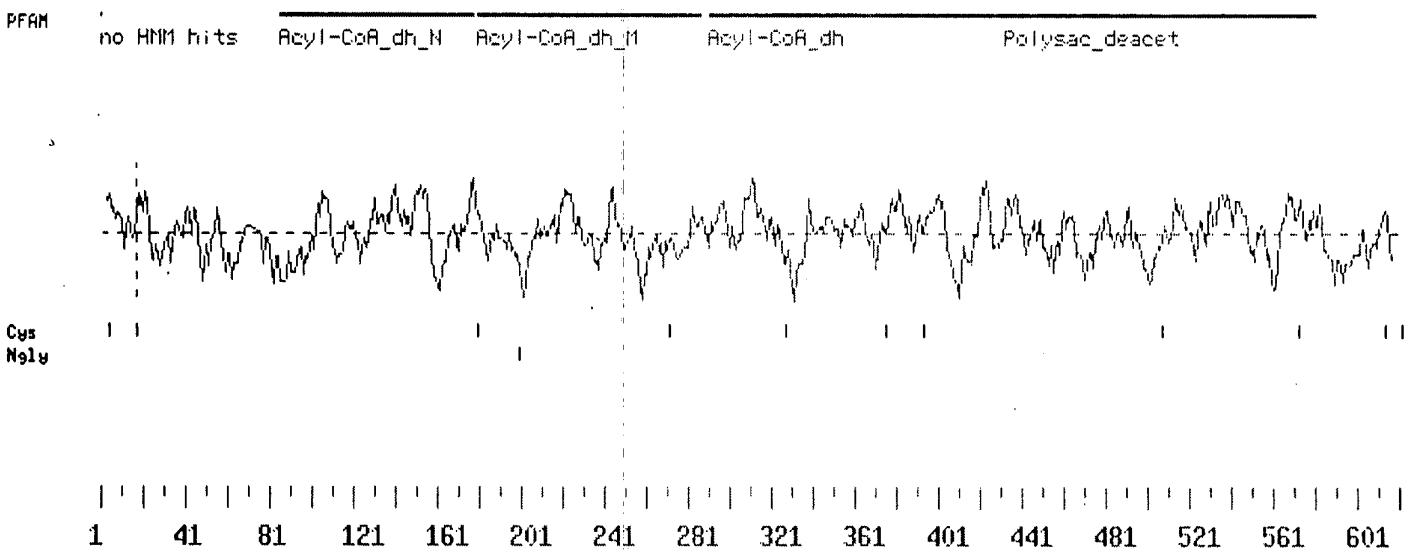


FIGURE 5